

SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1) .. (18)

<223> rat NogoA_623-640

<400> 1

Ser	Tyr	Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu
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Glu Ala

<210> 2

<211> 221

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1) .. (221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

<400> 2

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
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Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30

Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val

130

135

140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
210 215 220

<210> 3

<211> 238

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1) .. (238)

<223> Light Chain of 11C7 with leader sequence

<400> 3

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Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu

115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 4

<211> 3919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (3579)

<223> Human NogoA

<400> 4

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1 5 10 15

ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag 96
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30

gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc 192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac 240
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc 288
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala

85	90	95	
gct ccc ccc gtc gcc ccg gag cgg cag ccg tct tgg gac ccg agc ccg			336
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro			
100	105	110	
gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc			384
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val			
115	120	125	
tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc			432
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro			
130	135	140	
cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc			480
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr			
145	150	155	160
ccg cca gcc ccg gct ccc gcc gcg ccc ccc tcc acc ccg gcc gcg ccc			528
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro			
165	170	175	
aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt			576
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu			
180	185	190	
cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac			624
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp			
195	200	205	
ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc			672
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe			
210	215	220	
cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct			720
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro			
225	230	235	240

ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca	768
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser	
245 250 255	
aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct	816
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala	
260 265 270	
tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat	864
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp	
275 280 285	
tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc	912
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe	
290 295 300	
agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg	960
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg	
305 310 315 320	
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt	1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser	
325 330 335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa	1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys	
340 345 350	
ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt	1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser	
355 360 365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat	1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr	
370 375 380	

gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag	1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys	
385 390 395 400	
gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg	1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu	
405 410 415	
gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act	1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr	
420 425 430	
aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc	1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro	
435 440 445	
agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt	1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys	
450 455 460	
gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt	1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe	
465 470 475 480	
cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa	1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys	
485 490 495	
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc	1536
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr	
500 505 510	
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat	1584
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp	
515 520 525	
tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca	1632

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala	
530	540
aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa	1680
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu	
545	555
agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa	1728
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys	
565	575
atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct	1776
Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro	
580	590
gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca	1824
Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser	
595	605
cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt	1872
Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val	
610	620
cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa	1920
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu	
625	635
gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc	1968
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro	
645	655
cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga	2016
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly	
660	670
ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa	2064
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln	

675	680	685	
gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa			2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu			
690	695	700	
aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa			2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu			
705	710	715	720
atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa			2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu			
725	730	735	
gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca			2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser			
740	745	750	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa			2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys			
755	760	765	
gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat			2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn			
770	775	780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg			2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu			
785	790	795	800
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct			2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro			
805	810	815	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg			2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met			
820	825	830	

gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct	2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser	
835 840 845	
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca	2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro	
850 855 860	
att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat	2640
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp	
865 870 875 880	
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac	2688
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His	
885 890 895	
aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc	2736
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys	
900 905 910	
aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt	2784
Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val	
915 920 925	
gaa gag aaa atc agt ttc tca gat gac ttt tct aaa aat ggg tct gct	2832
Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala	
930 935 940	
aca tca aag gtg ctc tta ttg cct cca gat gtt tct gct ttg gcc act	2880
Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr	
945 950 955 960	
caa gca gag ata gag agc ata gtt aaa ccc aaa gtt ctt gtg aaa gaa	2928
Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu	
965 970 975	

gct gag aaa aaa ctt cct tcc gat aca gaa aaa gag gac aga tca cca	2976
Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro	
980 985 990	
tct gct ata ttt tca gca gag ctg agt aaa act tca gtt gtt gac ctc	3024
Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu	
995 1000 1005	
ctg tac tgg aga gac att aag aag act gga gtg gtg ttt ggt gcc	3069
Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala	
1010 1015 1020	
agc cta ttc ctg ctg ctt tca ttg aca gta ttc agc att gtg agc	3114
Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser	
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gta aca gcc tac att gcc ttg gcc ctg ctc tct gtg acc atc agc	3159
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser	
1040 1045 1050	
ttt agg ata tac aag ggt gtg atc caa gct atc cag aaa tca gat	3204
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp	
1055 1060 1065	
gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa gtt gct ata	3249
Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile	
1070 1075 1080	
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Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His	
1085 1090 1095	
gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt gat	3339
Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp	
1100 1105 1110	
gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt	3384

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe	
1115 1120 1125	
acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg	3429
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu	
1130 1135 1140	
gct ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat	3474
Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His	
1145 1150 1155	
cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt	3519
Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val	
1160 1165 1170	
aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag	3564
Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys	
1175 1180 1185	
cgc aaa gct gaa tga aaacgcccac aataattagt aggagttcat ctttaaaggg	3619
Arg Lys Ala Glu	
1190	
gatattcatt tgattatacy ggggaggggc agggaagaac gaaccttgac gttgcagtgc	3679
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taaaccgtaa tcatatcttt ttcctatctg aggcactggt ggaataaaaa acctgtatat	3859
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<211> 1192

<212> PRT

<213> Homo sapiens

<400> 5

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
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35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu

405	410	415
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr		
420	425	430
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro		
435	440	445
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys		
450	455	460
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe		
465	470	475
480		
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys		
485	490	495
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr		
500	505	510
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp		
515	520	525
Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala		
530	535	540
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu		
545	550	555
560		

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu

995	1000	1005
Leu Tyr Trp Arg Asp Ile Lys	Lys Thr Gly Val Val	Phe Gly Ala
1010	1015	1020
Ser Leu Phe Leu Leu Leu Ser	Leu Thr Val Phe Ser	Ile Val Ser
1025	1030	1035
Val Thr Ala Tyr Ile Ala Leu	Ala Leu Leu Ser Val	Thr Ile Ser
1040	1045	1050
Phe Arg Ile Tyr Lys Gly Val	Ile Gln Ala Ile Gln	Lys Ser Asp
1055	1060	1065
Glu Gly His Pro Phe Arg Ala	Tyr Leu Glu Ser Glu	Val Ala Ile
1070	1075	1080
Ser Glu Glu Leu Val Gln Lys	Tyr Ser Asn Ser Ala	Leu Gly His
1085	1090	1095
Val Asn Cys Thr Ile Lys Glu	Leu Arg Arg Leu Phe	Leu Val Asp
1100	1105	1110
Asp Leu Val Asp Ser Leu Lys	Phe Ala Val Leu Met	Trp Val Phe
1115	1120	1125
Thr Tyr Val Gly Ala Leu Phe	Asn Gly Leu Thr Leu	Leu Ile Leu
1130	1135	1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
1175 1180 1185

Arg Lys Ala Glu
1190

<210> 6

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (18)

<223> Human NogoA_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

<210> 7

<211> 819

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(819)

<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg
1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile
20 25 30

Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
805 810 815

Lys Thr Ser

<210> 8

<211> 10

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (10)

<223> hypervariable part of heavy chain of 11C7

<400> 8

Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(17)

<223> hypervariable part of heavy chain of 11C7

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 10

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of heavy chain of 11C7

<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr

1

5

<210> 11

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (16)

<223> hypervariable part of light chain of 11C7

<400> 11

Lys	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 13

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (9)

<223> hypervariable part of light chain of 11C7

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr
1 5

<210> 14

<211> 30

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (30)

<223> DNA-CDR1-11C7

<400> 14

ggattcgatt ttagaagaaa ttggatgagt

30

<210> 15

<211> 51

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (51)

<223> DNA-CDR2-11C7

<400> 15

gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> 16

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (27)

<223> DNA-CDR3-11C7

<400> 16

ccggtctgga tgtatgctat ggactac 27

<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (48)

<223> DNA-CDR'1-11C7

<400> 17

aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat

48

<210> 18

<211> 21

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (21)

<223> DNA-CDR'2-11C7

<400> 18

ctggtgtcta aactggactc t

21

<210> 19

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (27)

<223> DNA-CDR'3-11C7

<400> 19

tggcaaggta cacattttcc tcagacg

27

<210> 20

<211> 54

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1) .. (54)

<223> leader sequence for heavy chain of 11C7

<400> 20

atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val

1 5 10 15

cag tgt 54

Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

Gln Cys

<210> 22

<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1) .. (57)

<223> leader sequence for 11C7-light chain

<400> 22

atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

acc agc ggt

57

Thr Ser Gly

<210> 23

<211> 19

<212> PRT

<213> Mus musculus

<400> 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu

1

5

10

15

Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (181)

<223> human Nig-D20

<400> 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile

115

120

125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro

130

135

140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro

145

150

155

160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu

165

170

175

Pro Val Asp Leu Phe

180

<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1) .. (3492)

<223> rat NogoA

<400> 25

atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc acg gac agc 48
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc . 96
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro .
20 25 30

gag gag gag gag gag gag gag gag gag gag gag gag gag gag gag 144
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac 240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc 288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

gag ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc 336
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc ctg ccc tcc 384
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg cct ccg ccg	432
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro	
130 135 140	
cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc cct tcc acg	480
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr	
145 150 155 160	
ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat gag acc ctt	528
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu	
165 170 175	
ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa	576
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu	
180 185 190	
aaa att atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt	624
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly	
195 200 205	
caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct	672
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro	
210 215 220	
tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat gga tac ctt	720
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu	
225 230 235 240	
ggt aac tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act	768
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr	
245 250 255	
tta aat gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt	816
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe	
260 265 270	
gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg	864

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met	
275 280 285	
gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta	912
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val	
290 295 300	
gaa aac act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat	960
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp	
305 310 315 320	
tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt	1008
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly	
325 330 335	
aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat	1056
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn	
340 345 350	
gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac	1104
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp	
355 360 365	
ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga	1152
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly	
370 375 380	
agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac	1200
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp	
385 390 395 400	
aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat	1248
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp	
405 410 415	
agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct	1296
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro	

420	425	430	
gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca			1344
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser			
435	440	445	
gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat			1392
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His			
450	455	460	
act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc			1440
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala			
465	470	475	480
caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt			1488
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu			
485	490	495	
gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta			1536
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu			
500	505	510	
tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg			1584
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr			
515	520	525	
cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca			1632
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr			
530	535	540	
ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca			1680
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser			
545	550	555	560
gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca			1728
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser			
565	570	575	

ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt	1776
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val	
580 585 590	
atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta	1824
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val	
595 600 605	
gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat	1872
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr	
610 615 620	
gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc	1920
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala	
625 630 635 640	
atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag	1968
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu	
645 650 655	
cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata	2016
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile	
660 665 670	
tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca	2064
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro	
675 680 685	
agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg	2112
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser	
690 695 700	
gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa	2160
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu	
705 710 715 720	

cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca	2208
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr	
725 730 735	
caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct	2256
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser	
740 745 750	
gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag	2304
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln	
755 760 765	
gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt	2352
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser	
770 775 780	
aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag	2400
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu	
785 790 795 800	
aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat	2448
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn	
805 810 815	
gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca	2496
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr	
820 825 830	
ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt	2544
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe	
835 840 845	
gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat	2592
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp	
850 855 860	
cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca	2640

1010	1015	1020	
agc ttt	agg ata tat aag ggc	gtg atc cag gct atc	cag aaa tca 3114
Ser Phe	Arg Ile Tyr Lys Gly	Val Ile Gln Ala Ile	Gln Lys Ser
1025	1030	1035	
gat gaa	ggc cac cca ttc agg	gca tat tta gaa tct	gaa gtt gct 3159
Asp Glu	Gly His Pro Phe Arg	Ala Tyr Leu Glu Ser	Glu Val Ala
1040	1045	1050	
ata tca	gag gaa ttg gtt cag	aaa tac agt aat tct	gct ctt ggt 3204
Ile Ser	Glu Glu Leu Val Gln	Lys Tyr Ser Asn Ser	Ala Leu Gly
1055	1060	1065	
cat gtg	aac agc aca ata aaa	gaa ctg agg cgg ctt	ttc tta gtt 3249
His Val	Asn Ser Thr Ile Lys	Glu Leu Arg Arg Leu	Phe Leu Val
1070	1075	1080	
gat gat	tta gtt gat tcc ctg	aag ttt gca gtg ttg	atg tgg gtg 3294
Asp Asp	Leu Val Asp Ser Leu	Lys Phe Ala Val Leu	Met Trp Val
1085	1090	1095	
ttt act	tat gtt ggt gcc ttg	ttc aat ggt ctg aca	cta ctg att 3339
Phe Thr	Tyr Val Gly Ala Leu	Phe Asn Gly Leu Thr	Leu Leu Ile
1100	1105	1110	
tta gct	ctg atc tca ctc ttc	agt att cct gtt att	tat gaa cgg 3384
Leu Ala	Leu Ile Ser Leu Phe	Ser Ile Pro Val Ile	Tyr Glu Arg
1115	1120	1125	
cat cag	gtg cag ata gat cat	tat cta gga ctt gca	aac aag agt 3429
His Gln	Val Gln Ile Asp His	Tyr Leu Gly Leu Ala	Asn Lys Ser
1130	1135	1140	
gtt aag	gat gcc atg gcc aaa	atc caa gca aaa atc	cct gga ttg 3474
Val Lys	Asp Ala Met Ala Lys	Ile Gln Ala Lys Ile	Pro Gly Leu
1145	1150	1155	

aag cgc aaa gca gat tga

3492

Lys Arg Lys Ala Asp

1160

<210> 26

<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
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Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly

370	375	380
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp		
385	390	395 400
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp		
	405	410 415
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro		
	420	425 430
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser		
	435	440 445
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His		
	450	455 460
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala		
465	470	475 480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu		
	485	490 495
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu		
	500	505 510
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr		
	515	520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro

675

680

685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser

690

695

700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu

705

710

715

720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr

725

730

735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser

740

745

750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln

755

760

765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser

770

775

780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu

785

790

795

800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn

805

810

815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
835 840 845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
 1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
 1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
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Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

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<220>

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Ser Thr Ile Lys Glu Leu Arg Arg Leu
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<223> Synthetic peptide

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Ser

<210> 29

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<210> 30

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<223> CA-NA-3R

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<212> DNA

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.27

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28

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<210> 36

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<212> DNA

<213> Artificial Sequence

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<223> 3' primer

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24

<210> 38

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<223> 3' primer 2

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<223> 5'-VH leader

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<210> 43

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<213> Mus musculus

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<222> (1) .. (663)

<223> DNA variable part of heavy chain 11C7

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tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgct gtacctgcaa      300
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cccccatctg tctatccact ggcccctgga tctgctgccc aaactaactc catggtgacc      480
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